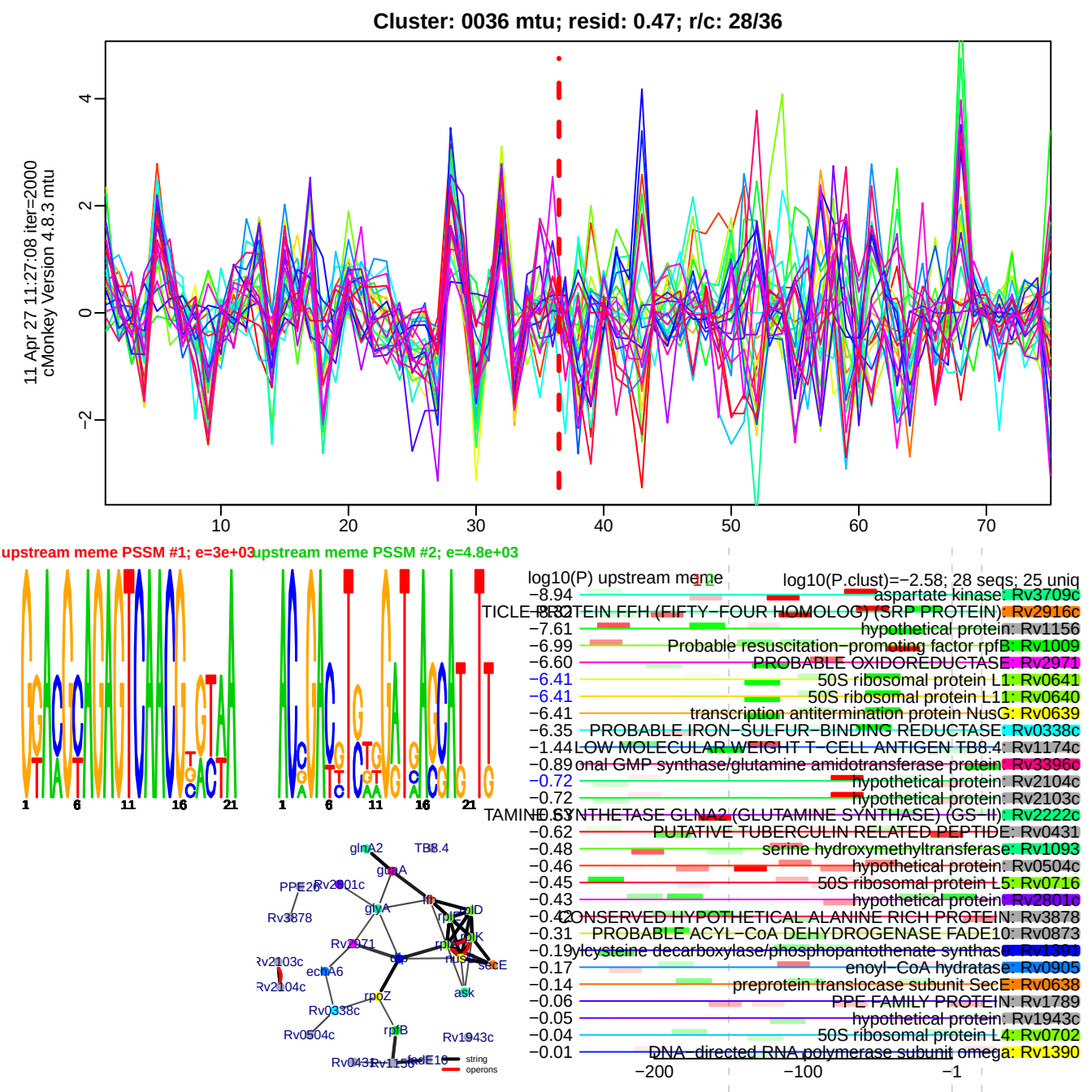
Cluster: 0036 mtu; resid: 0.47; r/c: 28/36
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=3e+03
upstream meme PSSM #2; e=4.8e+03
log10(P) upstream meme
log10(P.clust)=−2.58; 28 seqs; 25 uniq
−8.94 aspartate kinase: Rv3709c
TICLE-RESCUE PROTEIN FFH (FIFTY−FOUR HOMOLOG) (SRP PROTEIN): Rv2916c
−7.61 hypothetical protein: Rv1156
−6.99 Probable resuscitation−promoting factor rpfB: Rv1009
−6.60 PROBABLE OXIDOREDUCTASE: Rv2971
−6.41 50S ribosomal protein L1: Rv0641
−6.41 50S ribosomal protein L11: Rv0640
−6.41 transcription antitermination protein NusG: Rv0639
−6.35 PROBABLE IRON−SULFUR−BINDING REDUCTASE: Rv0338c
−1.44 LOW MOLECULAR WEIGHT T−CELL ANTIGEN TB8.4: Rv1174c
−0.89 onal GMP synthase/glutamine amidotransferase protein: Rv3396c
−0.72 hypothetical protein: Rv2104c
−0.72 hypothetical protein: Rv2103c
TAMINE SYNTHETASE GLNA2 (GLUTAMINE SYNTHASE) (GS−II): Rv2222c
−0.62 PUTATIVE TUBERCULIN RELATED PEPTIDE: Rv0431
−0.48 serine hydroxymethyltransferase: Rv1093
−0.46 hypothetical protein: Rv0504c
−0.45 50S ribosomal protein L5: Rv0716
−0.43 hypothetical protein: Rv2801c
−0.42 CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN: Rv3878
−0.31 PROBABLE ACYL−CoA DEHYDROGENASE FADE10: Rv0873
−0.19 ylcysteine decarboxylase/phosphopantothenate synthase: Rv1391
−0.17 enoyl−CoA hydratase: Rv0905
−0.14 preprotein translocase subunit SecE: Rv0638
−0.06 PPE FAMILY PROTEIN: Rv1789
−0.05 hypothetical protein: Rv1943c
−0.04 50S ribosomal protein L4: Rv0702
−0.01 DNA−directed RNA polymerase subunit omega: Rv1390
glnA2
TB8.4
PPE26
Rv2801c
Rv3878
Rv2971
Rv2103c
Rv2104c
Rv0338c
Rv0504c
Rv1943c
string
operons